```
GAATTCCGGCACGAGGCGGGTTGCAGTATGAGTCGCCAATCGGACCTAGTGAGGAGCTTCTTGGAGCAGCAGGAG          75
                         M  S  R  Q  S  D  L  V  R  S  F  L  E  Q  Q  E            16
GCCCGGGACCACCGGAAGGGGGCAATCCTCGCCCGTGAGTTCAGCGACATTAAGGCCCGCTCAGTGGGTTGGAAG          150
A  R  D  H  R  K  G  A  I  L  A  R  E  F  S  D  I  K  A  R  S  V  A  W  K           41
ACTGAAGGTGTGTGCTCCACTAAAGCCGGCAGTCAGCAGGGAAACTCAAAGAAGAACCGCTACAAAGACGTGGTA          225
T  E  G  V  C  S  T  K  A  G  S  Q  Q  G  N  S  K  K  N  R  Y  K  D  V  V           66
CCGTATGATGAGACGAGAGTCATCCTTTCCCTGCTCCAGGAGGAAGGACACGGAGATTACATTAATGCCAACTTC          300
P  Y  D  E  T  R  V  I  L  S  L  L  Q  E  E  G  H  G  D  Y  I  N  A  N  F           91
ATCCGGGGCACAGATGGAAGCCAGGCCTACATTGCGACGCAAGGACCCCTGCCTCACACTCTGTTGGACTTCTGG          375
I  R  G  T  D  G  S  Q  A  Y  I  A  T  Q  G  P  L  P  H  T  L  L  D  F  W          116
CGCCTGGTTTGGGAGTTTGGAATCAAGGTGATCTTGATGGCCTGTCAGGAGACAGAAAATGGACGGAGGAAGTGT          450
R  L  V  W  E  F  G  I  K  V  I  L  M  A  C  Q  E  T  E  N  G  R  R  K  C          141
GAACGCTACTGGGCCCAGGAGCGGGAGCCTCTACAGGCCGGGCCTTTCTGCATCACCCTGACAAAGGAGACAGCA          525
E  R  Y  W  A  Q  E  R  E  P  L  Q  A  G  P  F  C  I  T  L  T  K  E  T  A          166
CTGACTTCGGACATCACTCTCAGGACCCTCCAGGTTACATTCCAGAAGGAATCCCGTCCTGTGCACCAGCTACAG          600
L  T  S  D  I  T  L  R  T  L  Q  V  T  F  Q  K  E  S  R  P  V  H  Q  L  Q          191
TACATGTCTTGGCCGGACCACGGGGTTCCCAGCAGTTCCGATCACATTCTCACCATGGTGGAGGAGGCCCGTTGC          675
Y  M  S  W  P  D  H  G  V  P  S  S  S  D  H  I  L  T  M  V  E  E  A  R  C          216
CTCCAAGGACTTGGACCTGGACCCCTCTGTGTCCACTGCAGTGCTGGCTGTGGACGAACAGGTGTCTTGTGTGCT          750
L  Q  G  L  G  P  G  P  L  C  V  H  C  S  A  G  C  G  R  T  G  V  L  C  A          241
                                       ─────────────────────────────
CTCCAAGGACTTGGACCTGGACCCCTCTGTGTCCACTGCAGTGCTGGCTGTGGACGAACAGGTGTCTTGTGTGCT
GTTGATTACGTGAGGCAGTTGCTTCTGACTCAGACAATCCCACCCAATTTCAGCCTCTTTGAAGTGGTCCTGGAG          825
V  D  Y  V  R  Q  L  L  L  L  T  Q  T  I  P  P  N  F  S  L  F  E  V  -V  L  E      266
ATGCGGAAACAGCGACCTGCAGCGGTGCAGACAGAGGAGCAGTACAGGTTCCTGTACCACACAGTGGCTCAGCTA          900
M  R  K  Q  R  P  A  A  V  Q  T  E  E  Q  Y  R  F  L  Y  H  T  V  A  Q  L          291
TTCTCCCGCACTCTCCAGAACAACAGTCCCCTCTACCAGAACCTCAAGGAGAACCGCGCTCCAATCTGCAAGGAC          975
F  S  R  T  L  Q  N  N  S  P  L  Y  Q  N  L  K  E  N  R  A  P  I  C  K  D          316
TCCTCGTCCCTCAGGACCTCCTCAGCCCTGCCTGCCACATCCCGCCCACTGGGTGGCGTTCTCAGGAGCATCTCG          1050
S  S  S  L  R  T  S  S  A  L  P  A  T  S  R  P  L  G  G  V  L  R  S  I  S          341
GTGCCTGGGCCACCGACCCTTCCCATGGCTGACACTTACGCTGTGGTGCAGAAGCGTGGCGCTTCCGGCAGCACA          1125
V  P  G  P  P  T  L  P  M  A  D  T  Y  A  V  V  Q  K  R  G  A  S  G  S  T          366
GGGCCGGGCACGCGGGCGCCCAACAGCACGGACACCCCGATCTACAGCCAGGTGGCTCCACGTATCCAGCGGCCC          1200
G  P  G  T  R  A  P  N  S  T  D  T  P  I  Y  S  Q  V  A  P  R  I  Q  R  P          391
GTGTCACACACCGAAAACGCGCAGGGGACAACGGCACTGGGCCGAGTTCCTGCGGATGAAAACCCTTCCGGGCCT          1275
V  S  H  T  E  N  A  Q  G  T  T  A  L  G  R  V  P  A  D  E  N  P  S  G  P          416
GATGCCTATGAGGAAGTAACAGATGGAGCGCAGACTGGTGGGCTAGGCTTCAACTTGCGCATTGGAAGACCTAAA          1350
D  A  Y  E  E  V  T  D  G  A  Q  T  G  G  L  G  F  N  L  R  I  G  R  P  K          441
GGGCCACGGGATCCTCCAGCGGAGTGGACACGGGTGTAATGAGTGCTGTACCAGTTCCAGCCTGTCACTCAGTGG          1425
G  P  R  D  P  P  A  E  W  T  R  V  *                                             453
TGGCTGGGCGACTGCAACCCCCATGCTGCTGTGTGCTGTCTTATGTATGAGTGGGACTCATGGGCCTGAATCAAA          1500
ATAAAAGTTTCTCAGGGTAGAAAAAAAACAAATAGGGACTTTGGCCAGTGGTTATAGCAGTCAAAGCCAGGGGCTA          1575
GGAGGGGTAAGTGGGGGAGGTGGTGGATCTACTCTGAGAAAGTTTAGGAAAGCACATCAAGAGTGAGCATCGCCA          1650
CTCTTCTCCCCATACACCTACTGGAAAGTGCACCCCAGACAGAGTCCTAACTTGACAGTGCACCTCAGACAGGTC          1725
GCTACCTGGATGGACATGCTGGCCCTACAGCTAGAGACATGTCTAATTAGATCCTCATGTAAACTTGCAATGAGC          1800
TAGAAAGATCTCCGTCTGGTCAGGGAAATGGATCACCTAGTCAGGTAAATAGTGTGCCATCCAGAAGACAGAACT          1875
GCAAGATACCGTCTTTCTCAAAATGGAAGAAAATAGATCCTCAAACAAGTCAGGGTCTATATGACAGTTGTTCATCTAGTCAGTC      1950
GATCCTGCCCTGCCTCACTGCCATAATGTCACAAACAAGTCAGGGTCTATATGACAGTTGTTCATCTAGTCAGTC    2025
CTGACTGTGGCCTCTGCAGGCTCAGATAGTGCCTTCTGCAGACTCTTGGAATGCCCGTCTTGAACTTGATGAAAG        2100
CTTCTACCGGGAACTTGTAAACATCATTAAAATTATTAATGTAGAATTCAATAAAGAGTGGGTCAAAAACTCAAA       2175
AAAAAAAAAAAAAAAAAAAAAAAACTCGAGAGTACTTCTAGAGCGGGCGGG                                2226
```

Figure 1

Figure 2

Figure 3

```
                                                                   43
MCLK1   MRHSKRTYC-------PDWDERDWDYGTWRSSSSHKRKKKRSHSSAREQKR          50
MCLK2   P.PR.YHSSERGSRGSYHEHYQSRKHKRRR.R.WSSSSDRTRRR.REDS            47
MCLK3   H.C..YRSPEPDPYLTYRWK.RRS.SREHEGRLRYPSR.EPPPR.S---            42
MCLK4   .......H.---------...S.ESWGHESY.G-....__R......TQ.NRH


                                                                   91
MCLK1   CRYDHSKTTDSYYLESRSINEKAYHSRRYVDEY--RNDYMGYEPGHPYGE           93
MCLK2   YHVRSRSSY.DHSSDR.LY-------D.RYCGSYR....SRDRGEAY.DT           94
MCLK3   SRE.APYRTRKHAHHCHK.RTRSCSSASSRSQQSSKRSSR---------..          91
MCLK4   _KPH.QFKDSDCHYLEARCLNERDYRD.RYIDEY-....CEGYVPRH.HR


                                                                  140
MCLK1   PGSRYQMHS-SKSSGRSGRSSYKSKHRSRHHTSQHHSDGHSHRRKRSRSV          142
MCLK2   DFRQSYEYHREN..Y..Q...RRKHR.R.RRSRTFSRSSSHSS.RAK-..          136
MCLK3   SRE.APYRTRKHAHHCHK.RTRSCSSASSRSQQSSKRSSR---------..         139
MCLK4   DVESTYRIHC....V..R...P.R.RNRPCASH.S.----.......I


                                 >                                190
MCLK1   EDDEEGHLICQSGDVLSARYEIVDTLGEGAFGKVVECIDHKVGGRRVAVK          192
MCLK2   ...A.....YHV..W.QE.....S......TS.R..Q...RR..T...L.          186
MCLK3   ...K....V.RI.SW.QE.....GN....T.......L..ARGKSQ..L.          189
MCLK4   ...................R..........................


                                                                  240
MCLK1   IVKNVDRYCEAAQSEIQVLEHLNTTDPHSTFRCVQMLEWFEHRGHICIVF          242
MCLK2   .I...EK.K...RL..N...KI.EK..KNKNL....FD..DYH..M..S.          236
MCLK3   .IR..GH.R...RL..N..KKIKEK.KENK.L..L.SD.NFH..M..A.          239
MCLK4   .....GG.R...R.........S...N.V..........D.H..V....


                                                                  290
MCLK1   ELLGLSTYDFIKENSFLPFRMDHIRKMAYQICKSVNFLHSNKLTHTDLKP          292
MCLK2   ......F..L.D.NY..YPIHQV.H..F.L.QA.K...D..........          286
MCLK3   ....KN.FE.L...N.Q.YPLP.V.H....L.HALR...E.Q.......          289
MCLK4   ................QI....Q.....Q.I....H..........


                                                                  340
MCLK1   ENILFVKSDYTEANPKMKRDERTIVNPDIKVVDFGSATYDDEHHSTLVS          342
MCLK2   ......N...ELT..LEK.....SVKSTAVR........F.H.....I..          336
MCLK3   ......N..EFETL..EHKSCE.KSVK.TSIR.A......F.H...T.I.A          339
MCLK4   .........VVK..S........LK.T.............****


                                                                  390
MCLK1   TRHYRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFPTHDSREHLAMM          392
MCLK2   ............E.............IF...V...L.Q...N.......          386
MCLK3   .....P....E...A.............F..R...L.Q....K......          389
MCLK4   ...................................Q....K......


        **                                                        440
MCLK1   ERILGPLPKHMIQKTRKRRYFHHDRLDWDEHSSAGRYVSRRCKPLKEFML          442
MCLK2   ......V.SR..R....QK..YRG......NT......REN....RRYLT          436
MCLK3   .K....I.S....HR...QK..YKGG.V...N..D....KEN.....SY..         439
MCLK4   ......I.A.........K....NQ..............R.........


                                            <                     483
MCLK1   SQDAEHEFLFDLVGKILEYDPAKRITLKEALKHPFFYPLKKHT                 492
MCLK2   .EAED.HQ....IENM...E....L..G...Q....AC.RTEPPNTKLWD          486
MCLK4   QDSL..VQ....MRRM..F...Q....A...L....AG.TPEERSFHSSSR         489
MCLK5   CHDE...K.....RRM......R....D...Q....DL..RK


                                                                  499
MCLK1                                                              496
MCLK2   SSRDISR
MCLK3   NPSR
MCLK4
```

FIGURE 4

SIRP4   MEPAGPAPGRLGPLLCLLLAASCAWSGVAGEEELQVIQPDKSVSVAAGESAILHCTVT   58
SIRP1   MPVPASWPHLPSPFLLMTLLLGRLTGVAGEDELQVIQPEKSVSVAAGESATLRCAMT   57

4   SLIPVGPIQWFRGAGPARELIYNQKEGHFPRVTTVSESTKRENMDFSISISNITPADA   116
1   SLIPVGPIMWFRGAGAGRELIYNQKEGHFPRVTTVSELTKRNNLNFSISISNITPADA   115

4   GTYYCVKFRKGSPDT-EFKSGAGTELSVRAKPSAPVVSGPAARATEQHTVSFTCESHG   173
1   GTYYCVKFRKGSPDDVEFKSGAGTELSVRAKPSAPVVSGPAVRATEPHTVSFTCESHG   173

4   FSPRDITLKWFKNGNELSDFQTNVDRVGESVSYSIHSTAKVVLTREDVHSQVICEVAH   231
1   FSPRDITLKWFKNGNELSDFQTNVDRAGDSVSYSIHSTARVVLTRGDVHSQVICEMAH   231

4   VTLQGDPLRGTANLSETIRVPPTLEVTQQEVRAENQVNVTCQVRKFYPQRLQLTWLEN   289
1   ITLQGDPLRGTANLSEAIRVPPTLEVTQQFMRAENQANVTCQVSNFYERGLQLTWLEN   289

4   GNVSRTETASTVTENKDGTYNWMSWLLVNVSAHRDDVKLTCQVEHDGQPAVSKSHDLK   347
1   GNVSRTETASTLIENKDGTYNWMSWLLVNTCAHRDDVVLTCQVEHDGQCAVSKSYALE   347

4   VSAHPKEQGSNTAAENTGSNERNIYIVVGVVCTLLVALLMAALYLVRIRQKKAQGSTS   405
1   ISAHQKEHGSDITHEPALAPTAPLLVALLLGPKLLLVVGVSAIYICWKQKA   398

4   STRLHEPEKNAREITQDTNDI*TYADL*NLPKGKKPAPQAAEPNNHTEYASIQTSPQPAS   463

4   EDTL*TYADL*DMVHLNRTPKQPAPKPEPSFSEYASVQVPRK   503

Figure 5